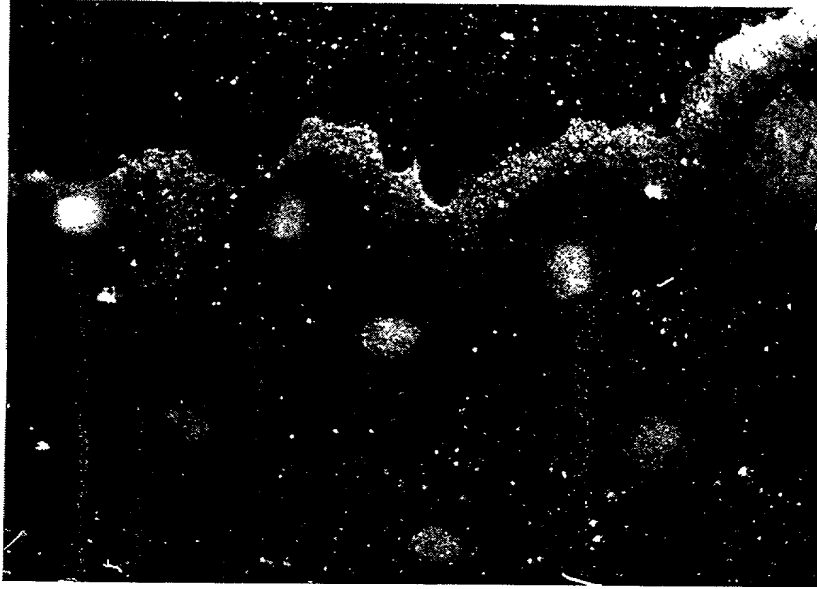
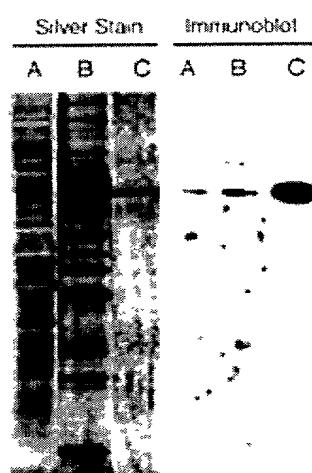


**Figure 1**



Bcap73 localizes to the forefront of endothelial cells migrating in response to injury.

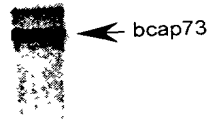
**Figure 2**



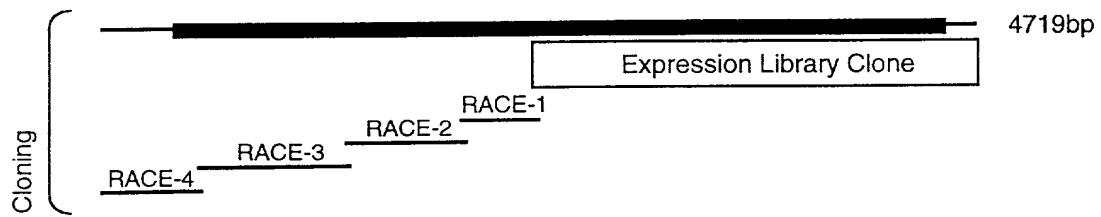
Bcap73 purification by ion-exchange chromatography.

**Figure 3**

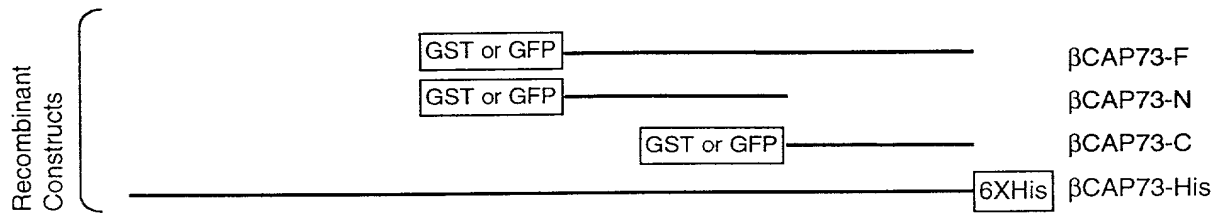
**A**



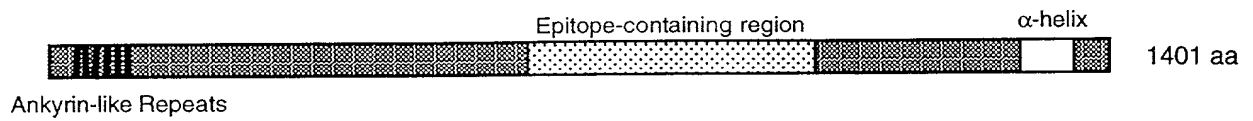
**B**



**C**



**D**



**Figure 4-1**

```
cagtgttgag gcggcaggat gtagagtgc tttcaagctt tccagtggag tccccgaaaa 60
gggaaggcag agaaagacat cttctaaata acaaataagga ggagttacag tacctgactt 120
ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180
gcggagaagg attccgaaga cgaagaaaaat atccttagag atccaagcta agtgtagtgc 240
agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagtttagga 300
gtctctctga gggctggctt tgtgagccac agtgatttgt aacttaatgc gaactaattt 360
gctgttagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412
                               Met Met Ser Cys Trp Phe Ser
                               1                               5

tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460
Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp
                               10                               20

cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508
Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser
                               25                               30                               35

atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556
Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly
                               40                               45                               50                               55

aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604
Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu
                               60                               65                               70

aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652
Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Thr Ser Asp Thr Ala
                               75                               80                               85

gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt 700
Gly Arg Asn Ala Leu His Leu Ala Ala Lys Tyr Gly His Ala Leu Cys
                               90                               95                               100

cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748
Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu
                               105                               110                               115

cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct 796
Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser
                               120                               125                               130                               135

agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844
Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp
                               140                               145                               150
```

gagcgtggtgag gcggcaggat gtagagtgc tttcaagctt tccagtggag tccccgaaaa 60  
gggaaggcag agaaagacat cttctaaata acaaataagga ggagttacag tacctgactt 120  
ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180  
gcggagaagg attccgaaga cgaagaaaaat atccttagag atccaagcta agtgtagtgc 240  
agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagtttagga 300  
gtctctctga gggctggctt tgtgagccac agtgatttgt aacttaatgc gaactaattt 360  
gctgttagca acaagaaact aaatcctgtc t atg atg agc tgt tgg ttt tct 412  
Met Met Ser Cys Trp Phe Ser 1 5  
tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac 460  
Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp 10 20  
cga ttg atg aga gca gca gaa agg gga gat gta gaa aaa gtg tcc tca 508  
Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser 25 30 35  
atc ctt gct aaa aag gga gtc aat cca ggc aag cta gat gta gaa ggc 556  
Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly 40 45 50 55  
aga tct gcc ttt cat gtt gtg gcc tca aag gga aat ctt gag tgt ttg 604  
Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu 60 65 70  
aat gcc atc ctc ata cat gga gtt gat att aca acc agt gac acc gca 652  
Asn Ala Ile Leu Ile His Gly Val Asp Ile Thr Thr Ser Asp Thr Ala 75 80 85  
gga agg aat gct ctt cac ctg gct gca aag tat ggg cat gca ctg tgt 700  
Gly Arg Asn Ala Leu His Leu Ala Ala Lys Tyr Gly His Ala Leu Cys 90 95 100  
cta caa aaa ctt cta cag tac aat tgt ccc act gaa cat gta gac ctg 748  
Leu Gln Lys Leu Leu Gln Tyr Asn Cys Pro Thr Glu His Val Asp Leu 105 110 115  
cag gga aga act gca ctt cat gat gca gct atg gca gac tgt cct tct 796  
Gln Gly Arg Thr Ala Leu His Asp Ala Ala Met Ala Asp Cys Pro Ser 120 125 130 135  
agc ata cag ctg ctc tgc gac cat ggg gcc tcg gtg aat gcc aaa gat 844  
Ser Ile Gln Leu Leu Cys Asp His Gly Ala Ser Val Asn Ala Lys Asp 140 145 150

**Figure 4-2**

gta gat ggg cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca	892
Val Asp Gly Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro	
155 160 165	
aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga	940
Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg	
170 175 180	
gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc	988
Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys	
185 190 195	
aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg	1036
Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu	
200 205 210 215	
ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac	1084
Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp	
220 225 230	
aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac	1132
Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn	
235 240 245	
aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat	1180
Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn	
250 255 260	
ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag	1228
Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu	
265 270 275	
cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag	1276
His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu	
280 285 290 295	
aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc	1324
Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val	
300 305 310	
aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat	1372
Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp	
315 320 325	
ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa	1420
Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu	
330 335 340	
aag cag cat gaa gaa agc cta aga act att gag gct ctg aaa agt aga	1468
Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg	
345 350 355	

gta gat ggg cgg aca cca ctt gtt ctg gct acc cag atg tgt agg cca  
 Val Asp Gly Arg Thr Pro Leu Val Leu Ala Thr Gln Met Cys Arg Pro  
 155 160 165  
 aca ata tgt caa ctg ctg ata gat aga ggg gcg gat att aat tcc aga  
 Thr Ile Cys Gln Leu Leu Ile Asp Arg Gly Ala Asp Ile Asn Ser Arg  
 170 175 180  
 gac aaa caa aac agg act gct ctc atg cta gga tgc gag tat ggt tgc  
 Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys  
 185 190 195  
 aaa gat gca gta gaa gtc tta atc aaa aac ggc gct gac gtg acc ttg  
 Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu  
 200 205 210 215  
 ctg gac gcc ctt ggc cat gac agt tct tac tat gca aga att ggt gac  
 Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp  
 220 225 230  
 aat ctg gac att cta acc tta ctg aag act gca tca gaa aat tcc aac  
 Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn  
 235 240 245  
 aaa ggg aga gaa ctt tgg aag aaa gga cca tct tta caa cag cga aat  
 Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn  
 250 255 260  
 ttg tct cag atg cta gat gaa gta aat acg aag tca aat cag agg gag  
 Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu  
 265 270 275  
 cat caa aac att cag gat ctg gag att gaa aat gaa gat ctg aaa gag  
 His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu  
 280 285 290 295  
 aga ttg aga aaa att cag caa gaa cag aga ata tta ttg gat aaa gtc  
 Arg Leu Arg Lys Ile Gln Gln Glu Gln Arg Ile Leu Leu Asp Lys Val  
 300 305 310  
 aat ggt tta cag cta cag ctg aat gag gaa gta atg gtg gct gat gat  
 Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp  
 315 320 325  
 ctg gaa agt gag aaa gaa aag ctg aag tcc ctt ttg gca gcc aaa gaa  
 Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu  
 330 335 340  
 aag cag cat gaa gaa agc cta aga act att gag gct ctg aaa agt aga  
 Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg  
 345 350 355

**Figure 4-3**

ttt aag tat ttt gag agt gat cat tta gga tca gga agt cat ttc agg	1516
Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg	
360 365 370 375	
aaa gaa gat atg ctt ctt aaa caa ggt caa atg tac atg aca gac tca	1564
Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser	
380 385 390	
cag tgt act tcc aca ggc atg cca gtc cat atg caa agc cga tct atg	1612
Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met	
395 400 405	
tta aga cca ctg gag cta gcc tta cct aat caa gcc tca tat tcg gaa	1660
Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu	
410 415 420	
aac gaa att tta aag aaa gaa tta gaa gca atg aga act ttc tgt gat	1708
Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp	
425 430 435	
tca gca aaa caa gac aga ctc aaa ctc caa aat gaa ctg gct cac aag	1756
Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys	
440 445 450 455	
gtg gcg gag tgc aag gcc tta gca ttg gaa tgt gaa agg gtg aaa gag	1804
Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu	
460 465 470	
gat tca gat gag cag ata aag caa cta gaa gat gcc ttg aaa gac gtg	1852
Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val	
475 480 485	
cag aag aga atg tat gag tcg gaa ggt aaa gtg aaa caa atg cag aca	1900
Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr	
490 495 500	
cat ttt ctt gcc ttg aaa gag cac ctg aca agt gat gcg gcc act ggg	1948
His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly	
505 510 515	
aac cac agg ctg atg gag gaa ctg aag gat cag ttg aaa gac atg aaa	1996
Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys	
520 525 530 535	
gtg aaa tac gaa ggt gcg tcc gca gaa gtg ggg aaa ttg aga aac caa	2044
Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln	
540 545 550	
atc aaa caa aat gaa atg tta gtt gaa gag ttt aag aga gat gag ggc	2092
Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly	
555 560 565	

1000 900 800 700 600 500 400 300 200 100 0

**Figure 4-4**

aag ctg atg gaa gag aat aag cga ctg cag aag gag ttg agc atg tgt	2140
Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys	
570 575 580	
gaa ctg gag cga gag aag aga gga agg aag ctc act gag atg gaa ggc	2188
Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly	
585 590 595	
cag tta aag gac ttg tca gcc aag ctg gcc ctt tct att cca gca gag	2236
Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu	
600 605 610 615	
aaa ttt gaa aac atg aag agc ttg tta tca aat gaa ctg aac gag aag	2284
Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys	
620 625 630	
gca aaa aaa tta ata gat gtg gaa aga gaa tat gaa aga tca ctt aat	2332
Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn	
635 640 645	
gaa act aga cca tta aag aga gaa ctt gag aat ttg aag gcc aaa ctg	2380
Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu	
650 655 660	
gct cag cac gtc aaa cca gag gaa cat gag cag ctc aag agc aga tta	2428
Ala Gln His Val Lys Pro Glu Glu His Glu Gln Leu Lys Ser Arg Leu	
665 670 675	
gag cag aag tca gga gaa ctt ggg aag agg atc act gag tta aca tcg	2476
Glu Gln Lys Ser Gly Glu Leu Gly Lys Arg Ile Thr Glu Leu Thr Ser	
680 685 690 695	
aaa aat cag acg tta caa aag gaa atc gaa aag gtc tgc ctg gat aat	2524
Lys Asn Gln Thr Leu Gln Lys Glu Ile Glu Lys Val Cys Leu Asp Asn	
700 705 710	
aag ctc ctt aca caa caa gta aat aac tta aca act gaa atg aaa aat	2572
Lys Leu Leu Thr Gln Gln Val Asn Asn Leu Thr Thr Glu Met Lys Asn	
715 720 725	
cat tac gtc cct tta aaa gta agt gaa gaa atg aaa aag tca cat gat	2620
His Tyr Val Pro Leu Lys Val Ser Glu Glu Met Lys Lys Ser His Asp	
730 735 740	
gta att gtt gat gat ttg aat aaa aag ctt tca gat gtg aca cac aaa	2668
Val Ile Val Asp Asp Leu Asn Lys Lys Leu Ser Asp Val Thr His Lys	
745 750 755	
tat aca gaa aag aag ttg gaa atg gag aag ttg ctt atg gaa aat gcc	2716
Tyr Thr Glu Lys Lys Leu Glu Met Glu Lys Leu Leu Met Glu Asn Ala	
760 765 770 775	

The amino acid sequence of the protein encoded by the DNA sequence shown above is:

**Figure 4-5**

agt tta agt aaa aat gtc agc cgc ctg gaa act gtg ttc ata cct ccc	2764
Ser Leu Ser Lys Asn Val Ser Arg Leu Glu Thr Val Phe Ile Pro Pro	
780 785 790	
gag aga cac gaa aaa gaa atg atg gct ctg aaa tcc aat atc act gaa	2812
Glu Arg His Glu Lys Glu Met Met Ala Leu Lys Ser Asn Ile Thr Glu	
795 800 805	
ctt aag aag cag ctg tct gaa ctt aat aaa aaa tgt ggt gaa gac caa	2860
Leu Lys Lys Gln Leu Ser Glu Leu Asn Lys Lys Cys Gly Glu Asp Gln	
810 815 820	
gag aaa ata tat tca ctc atg tct gaa aac aat gat ttg aaa aag acc	2908
Glu Lys Ile Tyr Ser Leu Met Ser Glu Asn Asn Asp Leu Lys Lys Thr	
825 830 835	
atg agt cat cag tat gtg ccc gtg aaa acc cat gaa gag att aaa act	2956
Met Ser His Gln Tyr Val Pro Val Lys Thr His Glu Glu Ile Lys Thr	
840 845 850 855	
gcc ttg agt agc aca ttg gat aaa acc aat aga gaa tta gta gat gtg	3004
Ala Leu Ser Ser Thr Leu Asp Lys Thr Asn Arg Glu Leu Val Asp Val	
860 865 870	
aag aag aag tgt gaa gat ata aat caa gaa ttt gtg aaa ata aaa gat	3052
Lys Lys Lys Cys Glu Asp Ile Asn Gln Glu Phe Val Lys Ile Lys Asp	
875 880 885	
gag aac gaa ata tta aaa aga aat ctg gag aac act cag aac caa gta	3100
Glu Asn Glu Ile Leu Lys Arg Asn Leu Glu Asn Thr Gln Asn Gln Val	
890 895 900	
aaa gct gag tac atc agc cta aga gag cat gaa gaa aag atg agt ggc	3148
Lys Ala Glu Tyr Ile Ser Leu Arg Glu His Glu Glu Lys Met Ser Gly	
905 910 915	
cta agg aag agc atg aag aag gtc cag gac aac agc gct gaa ata ctg	3196
Leu Arg Lys Ser Met Lys Lys Val Gln Asp Asn Ser Ala Glu Ile Leu	
920 925 930 935	
gct aag tac aaa aaa agc cag gag gag att gtc acc ctg cat gag gag	3244
Ala Lys Tyr Lys Lys Ser Gln Glu Glu Ile Val Thr Leu His Glu Glu	
940 945 950	
att gca gcc cag aag aga gaa ctc gac acg ata cag gaa tgc atc aag	3292
Ile Ala Ala Gln Lys Arg Glu Leu Asp Thr Ile Gln Glu Cys Ile Lys	
955 960 965	
cta aaa tat gct ccg atc atc agc ttg gaa gag tgt gag aga aaa ttt	3340
Leu Lys Tyr Ala Pro Ile Ile Ser Leu Glu Glu Cys Glu Arg Lys Phe	
970 975 980	

The amino acid sequence of the protein encoded by the cDNA was determined by mass spectrometry. The sequence is identical to that of the protein encoded by the cDNA.



[illegible]

aaa	gcc	act	gag	aaa	gaa	cta	aaa	gaa	cag	cta	tcc	cag	cag	aca	cag	3388
Lys	Ala	Thr	Glu	Lys	Glu	Leu	Lys	Glu	Gln	Leu	Ser	Gln	Gln	Thr	Gln	
	985					990					995					
aag	tat	aat	acc	agt	gaa	gaa	gag	gcc	aag	aag	tgc	aag	caa	gag	aat	3436
Lys	Tyr	Asn	Thr	Ser	Glu	Glu	Glu	Ala	Lys	Lys	Cys	Lys	Gln	Glu	Asn	
1000					1005					1010					1015	
gac	aag	tta	aag	aag	gag	atc	ctc	act	ctt	cag	aag	gat	cta	aag	gat	3484
Asp	Lys	Leu	Lys	Lys	Glu	Ile	Leu	Thr	Leu	Gln	Lys	Asp	Leu	Lys	Asp	
				1020					1025					1030		
aag	aat	gtt	cac	att	gag	aat	tct	tat	gaa	aca	gaa	aga	gca	tta	agc	3532
Lys	Asn	Val	His	Ile	Glu	Asn	Ser	Tyr	Glu	Thr	Glu	Arg	Ala	Leu	Ser	
			1035					1040					1045			
aga	aaa	aca	gaa	gag	ctg	aac	aga	cag	tta	aaa	gac	ctg	ttg	cag	aaa	3580
Arg	Lys	Thr	Glu	Glu	Leu	Asn	Arg	Gln	Leu	Lys	Asp	Leu	Leu	Gln	Lys	
		1050					1055					1060				
tac	aca	gag	gca	aag	aag	gag	aaa	gag	aag	ctc	gtg	gag	gaa	aat	gcc	3628
Tyr	Thr	Glu	Ala	Lys	Lys	Glu	Lys	Glu	Lys	Leu	Val	Glu	Glu	Asn	Ala	
		1065				1070					1075					
aag	cag	act	tct	gag	atc	ctt	gca	gca	caa	act	ctt	ttg	cag	aag	cag	3676
Lys	Gln	Thr	Ser	Glu	Ile	Leu	Ala	Ala	Gln	Thr	Leu	Leu	Gln	Lys	Gln	
1080					1085					1090					1095	
cat	gtt	ccg	ctg	gag	cag	gtt	gag	tcc	ctg	aaa	aaa	tct	ctt	agt	ggc	3724
His	Val	Pro	Leu	Glu	Gln	Val	Glu	Ser	Leu	Lys	Lys	Ser	Leu	Ser	Gly	
				1100					1105					1110		
aca	atc	gag	aca	ctc	aag	gaa	gaa	ctg	aaa	act	aag	cag	aga	tgt	tat	3772
Thr	Ile	Glu	Thr	Leu	Lys	Glu	Glu	Leu	Lys	Thr	Lys	Gln	Arg	Cys	Tyr	
			1115					1120					1125			
gag	aaa	gag	cag	cag	aca	gtg	acc	caa	ctg	cgg	cag	atg	ctg	gag	aat	3820
Glu	Lys	Glu	Gln	Gln	Thr	Val	Thr	Gln	Leu	Arg	Gln	Met	Leu	Glu	Asn	
		1130					1135					1140				
cag	aag	aac	tcc	tct	gtg	ccc	ctg	gct	gag	cat	ttg	cag	gtt	aag	gaa	3868
Gln	Lys	Asn	Ser	Ser	Val	Pro	Leu	Ala	Glu	His	Leu	Gln	Val	Lys	Glu	
		1145				1150					1155					
gca	ttt	gag	aaa	gaa	gtt	gga	atc	ata	aaa	gct	agc	ttg	aga	gaa	aag	3916
Ala	Phe	Glu	Lys	Glu	Val	Gly	Ile	Ile	Lys	Ala	Ser	Leu	Arg	Glu	Lys	
1160					1165					1170					1175	
gaa	gaa	gaa	agc	caa	aac	aaa	act	gaa	gag	gtc	tcc	aaa	ctc	cag	tct	3964
Glu	Glu	Glu	Ser	Gln	Asn	Lys	Thr	Glu	Glu	Val	Ser	Lys	Leu	Gln	Ser	
				1180					1185					1190		

**Figure 4-7**

gag att cag aat act aaa caa gcg tta aaa aaa tta gag act cgg gag	4012
Glu Ile Gln Asn Thr Lys Gln Ala Leu Lys Lys Leu Glu Thr Arg Glu	
1195 1200 1205	
gtg gtt gat ttg tcg aaa tat aaa gca acg aaa agc gat ttg gag aca	4060
Val Val Asp Leu Ser Lys Tyr Lys Ala Thr Lys Ser Asp Leu Glu Thr	
1210 1215 1220	
cag att tcc gac tta aac gaa aaa ttg gcc aat ctg aat agg aag tat	4108
Gln Ile Ser Asp Leu Asn Glu Lys Leu Ala Asn Leu Asn Arg Lys Tyr	
1225 1230 1235	
gag gaa gta tgt gag gag gtt ttg cat gcc aaa aag aag gaa ctg tct	4156
Glu Glu Val Cys Glu Glu Val Leu His Ala Lys Lys Lys Glu Leu Ser	
1240 1245 1250 1255	
gct aaa gat gag aag gaa ttg ctc cat ttc agc ata gag caa gaa atc	4204
Ala Lys Asp Glu Lys Glu Leu Leu His Phe Ser Ile Glu Gln Glu Ile	
1260 1265 1270	
aaa gat cag cag gaa cga tgt gac aaa tcc tta aca acc atc acg gag	4252
Lys Asp Gln Gln Glu Arg Cys Asp Lys Ser Leu Thr Thr Ile Thr Glu	
1275 1280 1285	
cta cag aga aga ata cag gaa tct gcc aaa caa atc gaa gca aaa gat	4300
Leu Gln Arg Arg Ile Gln Glu Ser Ala Lys Gln Ile Glu Ala Lys Asp	
1290 1295 1300	
aat aag ata act gaa ctg ctc aat gat gtg gag aga tta aaa cag gcc	4348
Asn Lys Ile Thr Glu Leu Leu Asn Asp Val Glu Arg Leu Lys Gln Ala	
1305 1310 1315	
ctc aat ggc ctt tcc cag ctc acc tat gga agt ggg agt ccc agc aag	4396
Leu Asn Gly Leu Ser Gln Leu Thr Tyr Gly Ser Gly Ser Pro Ser Lys	
1320 1325 1330 1335	
agg cag agt cag ctg att gac agc ctg cag cag cag gtc agg tcc ctg	4444
Arg Gln Ser Gln Leu Ile Asp Ser Leu Gln Gln Gln Val Arg Ser Leu	
1340 1345 1350	
cag cag cag ctg gcg gat gcc gac aga cag cac caa gaa gta att gca	4492
Gln Gln Gln Leu Ala Asp Ala Asp Arg Gln His Gln Glu Val Ile Ala	
1355 1360 1365	
att tat cgg aca cac ctt ctt agt gct gca cag ggt cac atg gat gag	4540
Ile Tyr Arg Thr His Leu Leu Ser Ala Ala Gln Gly His Met Asp Glu	
1370 1375 1380	
gat gtg cag gcc gcc tta ctg cag atc ata cag atg cgg cag ggg ctc	4588
Asp Val Gln Ala Ala Leu Leu Gln Ile Ile Gln Met Arg Gln Gly Leu	
1385 1390 1395	

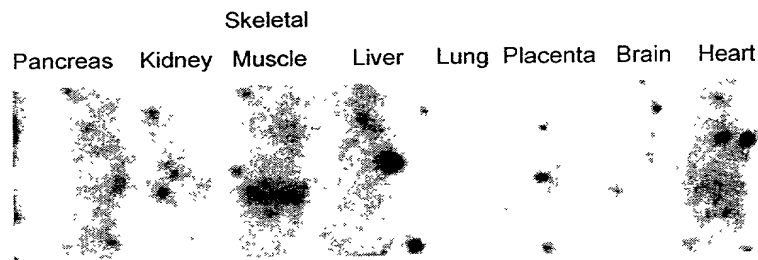
### Figure 4-8

```
gtg tgc tagtcggcac cccccagccc acagtggctt tccctgctgg tgctgagcat 4644
Val Cys
1400

tctgtgcgca acttcatggc ctttctgggc ctgctgtgc tagtataatt aaaataaagt 4704

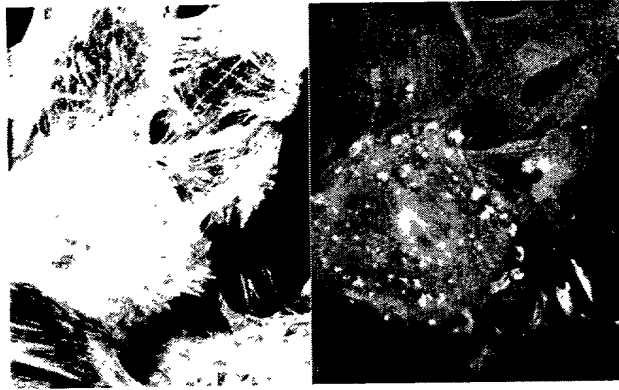
gtattttgat ccatcaaaaa aaaaaaaaaa aa 4736
```

**Figure 5**



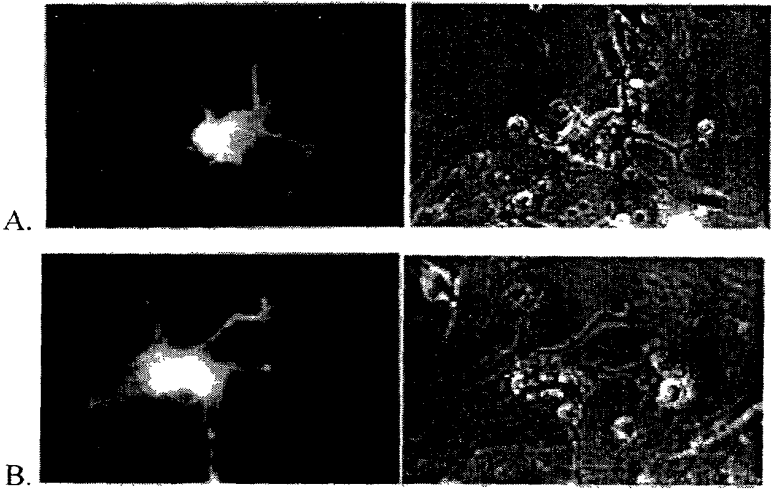
Bcap73 mRNA is expressed in various human tissues

**Figure 6**



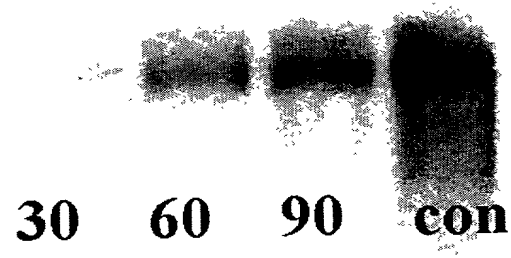
Overexpression of recombinant bcap73 induces formation of novel membrane protrusions

Figure 7



Overexpression of bcap73 domains induces aberrant cellular projections

**Figure 8**



Bcap73 mRNA is down-regulated in response to injury





Figure 9-2

Query: 898 atgtcaactgctgatagatagagggcgcatattaattccagagacaaacaaaacaggac 957  
|||||  
Sbjct: 552 ctgtcaactgctgatagatcgagggcgagagattaattccagagacaaacaaaacagaac 611

Query: 958 tgctctcatgctaggatgagagatgggtgcaaagatgcagtagaagtcttaataaaaaa 1017  
|||||  
Sbjct: 612 tgctctcatgcttggtgagagatgggtgtaaggatgctgtagaagtcttacttaaaaaa 671

Query: 1018 cggcgctgacgtgaccttgctggacgcccttgccatgacagttcttactatgcaagaat 1077  
|| |||||  
Sbjct: 672 tgggtgctgatgtaagcctgctggatgccttgggcatgtagttcttactatgcaagaat 731

Query: 1078 tggtgacaatctggacattctaacttactgaagactgcatcagaaaaattccaacaaagg 1137  
|||||  
Sbjct: 732 tggtgacaatctggacattctaactttattgaagactgcgtcagaaaaataccaacaaagg 791

Query: 1138 gagagaactttggaagaaaggaccatctttacaacagcgaaatttgctcagatgctaga 1197  
|||||  
Sbjct: 792 gagagaactttggaagaaaggaccatctttacagcagcgaaatttgccgtacatgctaga 851

Query: 1198 tgaagtaaatacgaagtcaaatacagaggagcatcaaacattcaggatctggagattga 1257  
|||||  
Sbjct: 852 tgaagtaaatacgaagtcaaatacagaggagcatcgaaacattcaggagctggagattga 911

Query: 1258 aaatgaagatctgaaagagagattgagaaaaattcagcaagaacagagaatattattgga 1317  
|||||  
Sbjct: 912 aaatgaagatttgaaagacaggttgagaaaaattcagcaagaacagagaatattactgga 971

Query: 1318 taaagtcaatgggtttacagctacagctgaatgaggaagtgaatgggtggctgatgatctgga 1377  
|||||  
Sbjct: 972 taaagtcaatgggtttacaactacagctgaatgaggaagtgaatgggttgctgatgatctgga 1031

Query: 1378 aagtgaagaaagaaaagctgaagtccttttggcagccaaagaaaagcagcatgaagaaag 1437  
|||||  
Sbjct: 1032 aagtgaagaaagaaaagctgaagtccttttgggtggctaaagaaaagcaacatgaagaaag 1091

Query: 1438 cctaagaactattgaggctctgaaaagtagatttaagtattttgag 1483  
|||||  
Sbjct: 1092 cctaagaactattgagtcctctgaaaacagatttaaatattttgag 1137

Figure 9-3

Query: 1566 agtgtacttccacaggcatgccagtcctatgcaaagccgatctatgttaagaccactgg 1625  
|||||  
Sbjct: 1136 agtgtacttccccaggggtgccagcccacatgcaaagcaggtctatgttaagaccactgg 1195

Query: 1626 agctagccttacctaatacaagcctcatattcggaaaacgaaattttaagaaagaattag 1685  
|||||  
Sbjct: 1196 agctatcattaccaatacaaacctcatattctgaaaatgacctcttaagaaagagttag 1255

Query: 1686 aagcaatgagaactttctgtgattcagcaaaacaagacagactcaaactccaaaatgaac 1745  
|||||  
Sbjct: 1256 aagcaatgagaactttctgcgaatcagccaaacaagaccgcctcaagctccagaacggag 1315

Query: 1746 tggctcacaaggtggcgagtgcaaggccttagcattggaatgtgaaaggtgaaagagg 1805  
|||||  
Sbjct: 1316 tggcgcaacaaggtggctgagtgcaaagctttaggactagaatgtgaacgcatcaaggagg 1375

Query: 1806 attcagatgagcagataaagcaactagaagatgccttgaaagacgtgcagaagagaatgt 1865  
|  
Sbjct: 1376 actctgatgagcagataaagcagttagaagacgcattgaaagatgtgcagaagagaatgt 1435

Query: 1866 atgagtcggaaggtaaagtgaacaaaatgcagacacattttctgccttgaaagagcacc 1925  
|||||  
Sbjct: 1436 atgagtcggaaggtaaagtgaacaaaatgcagacacactttctgccttgaaagagcacc 1495

Query: 1926 tgacaagtgatgcggccactgggaaccacaggctgatggaggaaactgaaggatcagttga 1985  
|||||  
Sbjct: 1496 tgaccagtgaagcagctataggaatcacagactaatggaggagctgaaggatcagttga 1555

Query: 1986 aagacatgaaagtgaatacgaaggtgcgtccgcagaagtggggaattgagaaaccaa 2045  
|  
Sbjct: 1556 aggacatgaaagcgaaatatgaggggtgcatcagcagaagtgggaaaactgcgaaaccaa 1615

Query: 2046 tcaaacaaaatgaaatgttagttgaagagtttaagagagatgagggcaagctgatggaag 2105  
|||||  
Sbjct: 1616 tcaaacaaaatgagctgctagtagaacagtttaggagagatgaaggcaagctggtggaag 1675

Query: 2106 agaataagcgactgcagaaggagttgagcatgtgtgaaactggagcgagagaagagaggaa 2165  
|||||  
Sbjct: 1676 agaataagcgattgcagaaggaaactcagtatgtgtgaaacggagcgagacaagaaaggaa 1735

Figure 9-4

```
Query: 2166 ggaagctcactgagatggaaggccagttaaaggacttgtcagccaagctggccctttcta 2225
          ||| | | ||||| ||||| ||||| ||||| | | ||| ||||| || | ||
Sbjct: 1736 ggaggggttgctgaggtggaaggccaggtaaaggaactcttagcaaagctgaccttgtcag 1795

Query: 2226 ttccagcagagaaatttgaaaacatgaagagcttggttatcaa 2267
          ||||| | || ||||| || | ||||| ||||| |||||
Sbjct: 1796 ttccaactgaaaaatttgagagcatgaagagcttattatcaa 1837
```

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**Figure 10-1**

Sequence Alignment of bcap73 against Tentative Human Concensus (THC) Contiguous Sequences  
THC244788 THC143090 THC186491 THC213238 (from TIGR)

Score = 1052 bits (547), Expect = 0.0

Identities = 905/1092 (82%), Positives = 905/1092 (82%), Gaps = 4/1092 (0%)

Query=bcap73 cDNA

Sbjct=THC seq

Query: 3136 aaagatgagtggcctaaggaagagcatgaagaaggtccaggacaacagcgctgaaatact 3195  
||||||| ||||| ||||||||| ||||| ||||| | | ||||||| |  
Sbjct: 6 aaagatgagctcgctaagtcagagcatgagaaaggtscaggatagtaatgctgaaatctt 65

Query: 3196 ggctaagtacnnnnnnngccaggaggagattgtcacccctgcatgaggagattgcagccca 3255  
||| | ||| ||||| || ||||||||| || ||||| || ||| |||||  
Sbjct: 66 ggccamctacagaaaaggccaagaagagattgtgacactkcatgccgaaattaragccca 125

Query: 3256 gaagagagaactcgacacgatacaggaatgcatcaagctaaaatatgctccgatcatcag 3315  
|| || || ||||||||| ||||| || ||||||| || ||||||||| || || |||||  
Sbjct: 126 gargarggagctcgacacaatacaagartgcattaaggtaaaatatgccccattgtcag 185

Query: 3316 cttggaagagtgtgagagaaaatttaaagccactgagaaagaac-taaaagaacagctat 3374  
||| || ||||| ||||||||| ||||| || ||||||||| ||||||| |||||  
Sbjct: 186 ctttgaggagtsctgagagaaaatttaaagcaacagagaaagaacctaaaagaccagttat 245

Query: 3375 cccagcagacacagaagtataataccagtgaagaagaggccaagaagtgaagcaagaga 3434  
| ||||||||| ||||||| | ||||||||| ||||||| |||||||||  
Sbjct: 246 cagagcagacacaaaagtatatgtgtcagtgaagaagaagtcaagaaaaacaagcaagaga 305

Query: 3435 atgacaagttaaagaaggagatcctcactcttcagaaggatctaaaggataagaatgttc 3494  
||||||||| ||||||||| || || ||||||||| ||| | | ||||| |||||  
Sbjct: 306 atgacaagttaaagaaggagatttttacccttcagaaagatttgagagayaagacagttc 365

Query: 3495 acattgagaattcttatgaaacagaaagagcattaagcagaaaaacagaagagctgaaca 3554  
||||||| || ||||||| ||||||||| ||||||||| ||||||| |||||  
Sbjct: 366 tcattgagaagtctcatgaaatggaaagagcattaagcagaaaaacagacgagctaaaca 425

Query: 3555 gacagttaaaagacctgttgcaaaatacacagaggcaaagaaggagaaagagaagctcg 3614  
||||||||| ||| ||||||||| || | ||||||| || |||||||||  
Sbjct: 426 aacagttaaaagacttgtcacagaaatacacggaagtaagaatgtgaaagagaagctag 485



**Figure 10-3**

```
Query: 4215 aggaacgatgtg 4226
      |||||
Sbjct: 1083 aggaacgatgtg 1094
```

Figure 10-3 shows a sequence alignment between a query sequence (4215-4226) and a subject sequence (1083-1094). The alignment is perfect, with 100% identity (10/10 matches) and 0% gaps. The sequences are: Query: 4215 aggaacgatgtg 4226 and Sbjct: 1083 aggaacgatgtg 1094.